AMENDMENTS TO THE CLAIMS

1. **(Currently Amended)** A method of identifying ~~a binding site domain having the capacity~~ at least one epitope binding domain capable of binding to a predetermined epitope ~~when positioned C-terminal of at least one second domain in a recombinant bi- or multivalent polypeptide comprising the steps of~~ comprising:

   (a) ~~testing a panel of binding site domains displayed~~ displaying on the surface of a biological display system ~~as part of a fusion protein for binding to a predetermined epitope, wherein said fusion protein comprises (1) a binding site domain, (2) a third domain positioned N-terminal of said binding site domain and (3)~~ a panel of bivalent or multivalent recombinant polypeptides comprised of (1) an N-terminal blocking domain at the N-terminus of said recombinant polypeptide, (2) a C-terminal anchoring domain ~~comprising an amino acid sequence~~ at the C-terminus of said recombinant polypeptide that mediates anchoring of ~~the fusion protein~~ said recombinant polypeptide to the surface of said display system, and (3) at least one epitope binding domain positioned between said N-terminal blocking domain and said C-terminal anchoring domain; and

   (b) identifying a ~~binding site domain that binds~~ subset of said recombinant polypeptides that bind to said predetermined epitope.

2. **(Currently Amended)** The method of claim 1, wherein said ~~binding site~~ N-terminal blocking domain and said ~~third~~ epitope binding domain are linked by a polypeptide linker~~disposed between said binding site and said third domain~~, wherein said polypeptide linker comprises a plurality of hydrophilic amino acids and connects the ~~C~~N-terminal end of said ~~binding site~~ blocking domain and the N~~C~~-terminal end of said ~~additional~~ epitope binding domain.

3. **(Currently Amended)** The method of claim 1 or 2, wherein said epitope binding ~~site~~domain is a pair of V_H-V_L, V_H-V_H or V_L-V_L domains.

4. **(Previously Presented)** The method of claim 1 wherein said display system is a filamentous phage produced by bacteria transfected therewith, a baculovirus expression system, a ribosome based expression system, a bacteriophage lambda display system or a bacterial surface expression system.

5. **(Currently Amended)** The method of claim 4 comprising, prior to step (a), the further step of

(a") transfecting bacteria with recombinant vectors encoding said ~~fucion proteins~~recombinant polypeptides.

6. **(Currently Amended)** The method of claim 1 comprising, prior to step (a"), the further step of

(a') cloning a panel of nucleic acid molecules encoding said epitope binding ~~site~~ domains into a vector.

7. **(Original)** The method of claim 6, wherein said panel of nucleic acid molecules is derived from immune competent cells of a mammal, fish or bird.

8. **(Currently Amended)** The method of claim 1, wherein said ~~third domain~~ N-terminal binding domain comprises at least 9 amino acids.

9. **(Currently Amended)** The method of claim 8, wherein said C-terminal anchoring ~~third~~ domain is or is derived from the N2-domain of the gene III product of filamentous phage.

10. **(Currently Amended)** The method of claim 1, wherein said ~~sequence that mediates said anchoring~~ C-terminal anchoring domain is or is derived from the C-terminal CT-domain of the gene III product of filamentous phage.

11. **(Previously Presented)** The method of claim 1, wherein said bi- or multivalent polypeptide is a bi- or multifunctional polypeptide.

12. **(Currently Amended)** The method of ~~claim 0~~claim 1, wherein said ~~at least one second~~ N-terminal blocking domain comprises ~~polypeptide selected from the group consisting of effector proteins~~ amino acid sequences that form an effector protein domain having a conformation suitable for biological activity, ~~amino acid sequences~~ capable of sequestering an ion, ~~and amino acid sequences capable~~ or capable of selective binding to a solid support.

13. **(Previously Presented)** The method of claim 12 wherein said effector protein is an enzyme, toxin, receptor, binding site, biosynthetic antibody binding site, growth factor, cell-differentiation factor, lymphokine, cytokine or hormone.

14. **(Original)** The method of claim 12 wherein said sequence capable of sequestering an ion is calmodulin, methallothionein, a fragment thereof, or an amino acid sequence rich in at least one of glutamic acid, aspartic acid, lysine, and arginine.

15. **(Original)** The method of claim 12 wherein said polypeptide sequence capable of selective binding to a solid support is a positively or negatively charged amino acid sequence, a cysteine-containing amino acid sequence, streptavidin, or a fragment of Staphylococcus protein A.

16. **(Original)** The method of claim 13, wherein said receptor is a co-stimulatory surface molecule important for T-cell activation or comprises an epitope binding site or a hormone binding site.

17. **(Original)** The method of claim 16, wherein said co-stimulatory surface molecule is CD80 (B7-1), CD86 (B7-2), CD58 (LFA-3) or CD54 (ICAM-1).

18. **(Cancelled)**

19. **(Previously Presented)** The method of claim 3, wherein said pair of domains are connected by a flexible linker, preferably by a polypeptide linker disposed between said domains, wherein said polypeptide linker comprises a plurality of hydrophilic amino acids of a length sufficient to span the distance between the C-terminal end of one of said domains and the N-terminal end of the other of said domains when said fusion protein assumes a conformation suitable for binding when disposed in aqueous solution.

20. **(Currently Amended)** The method of claim 1, wherein the identification of said binding site domain comprises the steps of

(b') removing said anchoring domain from said ~~fusion protein~~recombinant polypeptide;

(b") periplasmatically expressing the nucleic acid molecules encoding the remainder of said ~~fusion protein~~ recombinant polypeptide in bacteria; and

(b"') verifying whether said binding site domain binds to said predetermined epitope.

21. **(Currently Amended)** Kit comprising

(a) a panel of recombinant vectors encoding a panel of ~~fusion proteins~~ recombinant polypeptides as defined in any one of claims 1 to 20; and/or

(b) a bacterial library transfected with a panel of vectors as defined in (a).

22. **(Currently Amended)** A binding site domain or ~~fusion protein~~ recombinant polypeptide obtainable by the method of claim 1, wherein said binding site domain comprises at least one complementarity determining region (CDR) of the scFv fragment according to any one of ~~SEQ ID NOs.~~ SEQ ID Nos. 61, 63, 65, 67, 69, 71, 73, 75 and 77.

23. **(Original)** A polypeptide or an antibody comprising at least one binding site domain or fusion protein of claim 22.

24. **(Previously Presented)** The polypeptide or antibody of claim 23 having the amino acid sequence according to any one of ~~SEQ ID NOs~~SEQ ID Nos.. 61, 63, 65, 67, 69, 71, 73, 75 and 77.

25. **(Original)** Polynucleotides which upon expression encode the polypeptide or antibody of claim 23 or 24.

26. **(Original)** A cell transfected with a polynucleotide of claim 25.

27. **(Original)** A process for the preparation of a polypeptide or antibody of claim 23 or 24 comprising cultivating a cell of claim 26 under conditions suitable for the expression of the polypeptide and isolating the polypeptide from the cell culture medium.

28. **(Original)** A pharmaceutical composition containing a polypeptide or antibody of claim 23 or 24 and optionally a pharmaceutically acceptable carrier.

29. **(Original)** A diagnostic composition comprising the polypeptide or antibody of claim 23 or 24 and optionally suitable means for detection.

30. **(Currently Amended)** A binding site domain or ~~fusion protein~~ recombinant polypeptide obtainable by the method of claim 1, wherein said binding site domain or ~~fusion protein~~ recombinant polypeptide comprises at least one complementary determining region (CDR) of the scFv fragment ~~shown in figure 6.10.~~according to SEQ ID No. 75.

31. **(Currently Amended)** A polypeptide or an antibody comprising at least one binding site domain or ~~fusion protein~~ recombinant polypeptide of claim 30.

32. **(Previously Presented)** The polypeptide or antibody of claim 23, having the amino acid sequence according to SEQ ID No. 75.

33. **(Previously Presented)** The polypeptide of claim 32 having the amino acid sequence according to SEQ ID No. 75.

34. **(Currently Amended)** A polypeptide or an antibody comprising at least one binding site domain or ~~fusion protein~~ recombinant polypeptide that comprises any one of ~~SEQ ID NOs. SEQ ID NOs.~~SEQ ID Nos. 61, 63, 65, 67, 69, 71, 73, 75 and 77.

35. **(Currently Amended)** A polypeptide or an antibody comprising at least one binding site domain or fusion protein that comprises ~~SEQ ID NO. 75~~SEQ ID No. 75..

36. **(New)** The method of claim 1, wherein said epitope binding domain is comprised of at least two domains selected from the group consisting of V_H and V_L.